

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Tuesday, August 27, 2002 1:43 PM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 09/583848

Please rush. Thanks Chris

-----Original Message-----

From: Davis, Minh-Tam
Sent: Tuesday, August 27, 2002 1:25 PM
T : Chan, Christina
Subject: Rush search request for 09/583848

Please use the grandparent cases 08/967727 or 08/037230 for search
Please search in commercial database and in issued patent files:

1) Nucleotides 451-1156 of SEQ ID NO:18

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12
305-2008

Minh-Tam,
Seq ID 18, SN 08/967727 (Pat. no.
6025474) only 225 residues

Beverly
IEOS
C8-4994

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 09-05-02

Searcher: Beverly e4994

Terminal time: 20

Elapsed time: _____

CPU time: _____

Total time: 23

Number of Searches: _____

Number of Databases: 1

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

☒ Other CGN

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Davis, M.
091583848
Seq-ID 18

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 11:13:22 ; Search time 1922.63 Seconds
(without alignments)
2448.974 Million cell updates/sec

Title: US-08-967-727-18
Perfect score: 225
Sequence: 1 TATTTCTTTCCTGATCTT.....GGCACTGTGCCCTGAGGAG 225

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Length | ID | Description |
|------------|-------------|------------|-------|-------------|
| 1 | 100.0% | Score 225; | DB 6; | Length 225; |

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| 1 | 225 | 100.0 | 225 | 6 | AR153509 | Sequence 18 | 225 bp | DNA | linear | PAT 08-AUG-2001 |
| 2 | 225 | 100.0 | 225 | 6 | I36933 | Sequence 18 | | | | |
| 3 | 220.2 | 97.9 | 945 | 6 | AR167371 | Sequence 18 | | | | |
| 4 | 220.2 | 97.9 | 945 | 6 | HSU10339 | Human MAGE- | | | | |
| 5 | 220.2 | 97.9 | 1019 | 6 | AR167377 | Sequence 18 | | | | |
| 6 | 220.2 | 97.9 | 1019 | 9 | HUMMAGEB | D32076 Human mRNA | | | | |
| 7 | 220.2 | 97.9 | 1362 | 6 | AX019384 | Sequence 18 | | | | |
| 8 | 220.2 | 97.9 | 3871 | 9 | HSU10691 | Human MAGE- | | | | |
| 9 | 220.2 | 97.9 | 245077 | 9 | AF002997 | Homo sapi | | | | |
| 10 | 213.8 | 95.0 | 1212 | 6 | AX019380 | Sequence 18 | | | | |
| 11 | 213.8 | 95.0 | 1353 | 6 | AX019376 | Sequence 18 | | | | |
| 12 | 213.8 | 95.0 | 1569 | 6 | AX343855 | Sequence 18 | | | | |
| 13 | 213.8 | 95.0 | 1640 | 6 | AR153502 | Sequence 18 | | | | |
| 14 | 213.8 | 95.0 | 1640 | 6 | I36926 | Sequence 11 | | | | |
| 15 | 213.8 | 95.0 | 1663 | 9 | BC011744 | Homo sapi | | | | |
| 16 | 213.8 | 95.0 | 1709 | 9 | BC000340 | Homo sapi | | | | |
| 17 | 213.8 | 95.0 | 1710 | 9 | BC017389 | Homo sapi | | | | |
| 18 | 213.8 | 95.0 | 1715 | 9 | BC016803 | Homo sapi | | | | |
| 19 | 213.8 | 95.0 | 1753 | 9 | BC005963 | Homo sapi | | | | |
| 20 | 213.8 | 95.0 | 4204 | 6 | AR079453 | Sequence 18 | | | | |
| 21 | 213.8 | 95.0 | 4204 | 6 | AR167370 | Sequence 18 | | | | |
| 22 | 213.8 | 95.0 | 4204 | 6 | AR170361 | Sequence 18 | | | | |
| 23 | 213.8 | 95.0 | 4204 | 6 | AX333265 | Sequence 18 | | | | |
| 24 | 213.8 | 95.0 | 4204 | 9 | HS003735 | Human MAGE- | | | | |
| 25 | 213.8 | 95.0 | 245077 | 9 | AF002997 | Homo sapi | | | | |
| 26 | 213.8 | 95.0 | 289248 | 9 | U82671 | Homo sapi | | | | |
| 27 | 196.8 | 87.5 | 1678 | 9 | BC003408 | Homo sapi | | | | |
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| 29 | 195.2 | 86.8 | 1030 | 6 | AX328166 | Sequence 18 | | | | |
| 30 | 195.2 | 86.8 | 4157 | 6 | AR153500 | Sequence 18 | | | | |
| 31 | 195.2 | 86.8 | 4157 | 6 | I36924 | Sequence 9 | | | | |
| 32 | 195.2 | 86.8 | 4523 | 6 | AX119704 | Sequence 18 | | | | |
| 33 | 195.2 | 86.8 | 4523 | 9 | HUMMAGE12X | Human MAGE- | | | | |
| 34 | 195.2 | 86.8 | 4559 | 9 | AR167369 | Sequence 18 | | | | |
| 35 | 195.2 | 86.8 | 4559 | 9 | HUMMAGE2X | Human MAGE- | | | | |
| 36 | 195.2 | 86.8 | 289248 | 9 | U82671 | Homo sapi | | | | |
| 37 | 195.2 | 86.8 | 302250 | 6 | AX335531 | Sequence 18 | | | | |
| 38 | 195.2 | 86.8 | 302250 | 6 | AX335531 | Sequence 18 | | | | |
| 39 | 193.6 | 86.0 | 1657 | 9 | BC013098 | Homo sapi | | | | |
| 40 | 192 | 85.3 | 3295 | 2 | AC084372 | Homo sapi | | | | |
| 41 | 184 | 81.8 | 951 | 9 | AF443295 | Homo sapi | | | | |
| 42 | 163.2 | 72.5 | 1084 | 6 | AR052774 | Sequence 18 | | | | |
| 43 | 163.2 | 72.5 | 1094 | 6 | AR052773 | Sequence 18 | | | | |
| 44 | 163.2 | 72.5 | 1338 | 6 | AX019382 | Sequence 18 | | | | |
| 45 | 163.2 | 72.5 | 1341 | 6 | AX019377 | Sequence 18 | | | | |

ALIGNMENTS

| | | | | | | |
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| RESULT 1 | AR153509 | Sequence 18 from patent US 6235525. | 225 bp | DNA | linear | PAT 08-AUG-2001 |
| LOCUS | AR153509 | Sequence 18 from patent US 6235525. | | | | |
| DEFINITION | AR153509 | Sequence 18 from patent US 6235525. | | | | |
| ACCESSION | AR153509 | Sequence 18 from patent US 6235525. | | | | |
| VERSION | AR153509.1 | GI:15121041 | | | | |
| KEYWORDS | Unknown. | | | | | |
| SOURCE | Unknown. | | | | | |
| ORGANISM | Unclassified. | | | | | |
| REFERENCE | 1 (bases 1 to 225) | | | | | |
| AUTHORS | van den Eynde, B., van der Bruggen, P. and Boon-Falleur, T. | | | | | |
| TITLE | Isolated nucleic acid molecules coding for tumor rejection antigen precursor MAGE-3 and uses thereof | | | | | |
| JOURNAL | Patent: US 6235525-A 18 22-MAY-2001; | | | | | |
| FEATURES | location/Qualifiers | | | | | |
| source | 1..225 | | | | | |
| BASE COUNT | 44 a 65 c 58 g 58 t | | | | | |
| ORIGIN | /organism="unknown" | | | | | |

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Best Local Similarity 100.0%; Pred. No. 5.3e-43; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGGCACCTGCTGGGCCTC 120
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QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCACGACAGGCTTCTCTGATAATC 180
Db 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCACGACAGGCTTCTCTGATAATC 180
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QY 181 ATCCTGGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGTAGGAG 225
Db 181 ATCCTGGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGTAGGAG 225
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RESULT 2
LOCUS I36933 225 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 18 from patent US 5612201.
ACCESSION I36933
VERSION I36933.1 GI:2084893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS De Plaen,E., Boon-Falleur,T., Lethe,B., Szikora,J.-P., De Smet,C. and Chomez,P.
TITLE Isolated nucleic acid molecules useful in determining expression of a tumor rejection antigen precursor
JOURNAL Patent: US 5612201-A 18 18-MAR-1997;
FEATURES Location/Qualifiers
source 1..225
BASE COUNT 44 a 65 c 58 g 58 t
ORIGIN

Query Match 100.0%; Score 225; DB 6; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.3e-43;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGGCACCTGCTGGGCCTC 120
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QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCACGACAGGCTTCTCTGATAATC 180
Db 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCACGACAGGCTTCTCTGATAATC 180
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QY 181 ATCCTGGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGTAGGAG 225
Db 181 ATCCTGGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGTAGGAG 225
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RESULT 3
LOCUS AR167371 945 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 7 from patent US 6287569.
ACCESSION AR167371
VERSION AR167371.1 GI:17903147
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 945)
AUTHORS Kipps,T.J. and Wu,Y.
TITLE Vaccines with enhanced intracellular processing
JOURNAL Patent: US 6287569-A 7 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..945
BASE COUNT 213 a 254 c 275 g 203 t
ORIGIN

Query Match 97.9%; Score 220.2; DB 6; Length 945;
Best Local Similarity 98.7%; Pred. No. 6.9e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGGCACCTGCTGGGCCTC 120
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Db 493 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGGCACCTGCTGGGCCTC 552
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QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCACGACAGGCTTCTCTGATAATC 180
Db 553 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCACGACAGGCTTCTCTGATAATC 612
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QY 181 ATCTGTGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGTAGGAG 225
Db 613 ATCTGTGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGTAGGAG 657
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RESULT 4
LOCUS HSU10339 945 bp mRNA linear PRI 13-JUN-1994
DEFINITION Human MAGE-3b mRNA, complete cds.
ACCESSION U10339
VERSION U10339.1 GI:499121
KEYWORDS human.
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 945)
AUTHORS Fenton,R.G.
TITLE Cloning and Analysis of MAGE-1 Related Genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 945)
AUTHORS Fenton,R.G.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1994) Robert G. Fenton, BRMP, NCI-FCRDC, Frederick, MD 21702, USA
FEATURES Location/Qualifiers
source 1..945
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MAGE-3b"
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/cell_line="DM150"
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/dev_stage="adult"
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/product="MAGE-3b"
/protein_id="AAAI9006.1"
/db_xref="GI:499122"

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VFGIEMVEDPIGHVYIFATCLGLSYDGLLDNQIMPKTGLFLLIILAIITAKGDCAPE
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Best Local Similarity 98.7%; Pred. No. 6.9e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 433 TACTTCTTCTTCCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACGTGGTCTTTGGCATC 492
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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCCTC 120
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QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCACGACAGGCTTCCTGTATAATC 180
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Db 553 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCACGACAGGCTTCCTGTATAATC 612
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QY 181 ATCTGGCCATATCCAGAGAGGGCGACTGTGCCCTCGAGGAG 225
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Db 613 ATCTGGCCATATCCAGAGAGGGCGACTGTGCCCTCGAGGAG 657
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RESULT 5
AR167377 LOCUS AR167377 1019 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 13 from patent US 6287569.
ACCESSION AR167377
VERSION AR167377.1 GI:17903153
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1019)
AUTHORS Kipps,T.J. and Wu,Y.
TITLE Vaccines with enhanced intracellular processing
JOURNAL Patent: US 6287569-A 13 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..1019
/organism="unknown"

BASE COUNT 224 a 284 c 292 g 219 t
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Best Local Similarity 98.7%; Pred. No. 6.9e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCCTC 120
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Db 558 GAGCTGATGGAAGTGGACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCCTC 617
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QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCACGACAGGCTTCCTGTATAATC 180
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Db 618 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCACGACAGGCTTCCTGTATAATC 677
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QY 181 ATCTGGCCATATCCAGAGAGGGCGACTGTGCCCTCGAGGAG 225
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Db 678 ATCTGGCCATATCCAGAGAGGGCGACTGTGCCCTCGAGGAG 722
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RESULT 6
HUMMAGEB HUMMAGEB 1019 bp mRNA linear PRI 07-FEB-1999
LOCUS

DEFINITION Human mRNA for MAGE-6 protein, complete cds.
ACCESSION D32076
VERSION D32076.1 GI:1125015
KEYWORDS MAGE-6 protein; melanoma antigen.
SOURCE Homo sapiens cell-line M73 CDNA to mRNA.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1019)
AUTHORS Imai,Y.
TITLE Direct Submission
JOURNAL Submitted (08-JUL-1994) Yasuhisa Imai, Kurume University School of Medicine, Immunology; Asahi 67, Kurume, Fukuoka 830, Japan
(Tel:0942-31-7551, Fax:0942-31-7699)

REFERENCE 2 (bases 1 to 1019)
AUTHORS Imai,Y., Shichijo,S., Yamada,A., Katayama,T., Yano,H. and Itoh,K.
TITLE Sequence analysis of the MAGE gene family encoding human tumor-rejection antigens
JOURNAL Gene 160 (2), 287-290 (1995)
MEDLINE 95369706
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
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66..1010
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/note="Nomenclature of MAGE-6 was according to MAGE gene's 27 nucleotide sequences of HLA-A1 binding motif (Traversari et al., 1992)"
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/evidence=experimental
/product="MAGE-6 protein"
/protein_id="BAA06842.1"
/db_xref="GI:1125016"

CDS

BASE COUNT 224 a 284 c 292 g 219 t
ORIGIN
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Best Local Similarity 98.7%; Pred. No. 6.9e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTCTTCCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACGTGGTCTTTGGCATC 60
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Db 618 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCACGACAGGCTTCCTGTATAATC 677
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Db 678 ATCTGGCCATATCCAGAGAGGGCGACTGTGCCCTCGAGGAG 722
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RESULT 7
AX019384 LOCUS AX019384 1362 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9940188.
ACCESSION AX019384
VERSION AX019384.1 GI:10043354
KEYWORDS

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SOURCE          human.
ORGANISM         Homo sapiens
REFERENCE        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE           1 (bases 1 to 1362)
                Slaoui,M.M., Cohen,J., Cabezon,S.T. and Vinals,B.C.
                Tumor-associated antigen derivatives from the mage family, and
                nucleic acid sequences encoding them, used for the preparation of
                fusion proteins and of compositions for vaccination
                Patent: WO 9940188-A 10 12-AUG-1999;
                SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
                JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)
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                /db_xref="taxon:9606"
                /note="Melanoma tissue"
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ORIGIN
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Best Local Similarity 98.7%; Pred. No. 6.9e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 943 TCCACGATGGCTGCTGGGTGACAATCAGATCATGCCAGACAGGCTTCTTGATAATC 1002
|||
QY 181 ATCTGGCCATAATCGCAAGAGAGGCGACTGTGCCCTTGAGGAG 225
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Db 1003 ATCTGGCCATAATCGCAAGAGAGGCGACTGTGCCCTTGAGGAG 1047
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RESULT 8
HSU10691        3871 bp  DNA  linear  PRI 23-JUN-1995
LOCUS           Human MAGE-6 antigen (MAGE6) gene, complete cds.
DEFINITION      U10691
ACCESSION       U10691
VERSION         U10691.1 GI:533522
KEYWORDS        human.
SOURCE          human.
ORGANISM        Homo sapiens
REFERENCE        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE           1 (bases 1 to 3871)
                De Plaen,E., Arden,K., Traversari,C., Gaforio,J.J., Szikora,J.P.,
                De Smet,C., Brasseur,F., van der Bruggen,P., Lethe,B.,
                Lurquin,C.Brasseur.R., Chomez,P., De Backer,O., Cavenee,W. and
                Boon,T.
                Structure, chromosomal localization, and expression of 12 genes of
                the MAGE family
                Immunogenetics 40 (5), 360-369 (1994)
JOURNAL          95012457
MEDLINE          2 (bases 1 to 3871)
AUTHORS          De Plaen,E.
TITLE           Direct Submission
JOURNAL          Submitted (14-JUN-1994) Etienne De plaen, Ludwig Institute for
                Cancer Research, 74 Avenue Hippocrate, Brussels, 1200, Belgium
FEATURES
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                /organism="Homo sapiens"
                /isolate="patient M22"
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                /chromosome="X"

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2264..3208
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2264..3208
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/translation="MPLEQSRQHCPEEGLEARGALGLVGAQAPATEOEBAASSST
LV8VLTGEVPAAESPDPOGASSLPTTNNYPLWSQSYEDSSNQEEGSPFPDLE
SEFQAALSRKVALYHLLKYLKARREPVTKAEMLSGVVGNWQYFFVFIFSKASDLSL
VFGIELMEVDPIGHVYIFATCLGSLYDGLGDNQIMPTKLTGLIILAIITAKEGDCAPE
EKIWEELSVLEFEGREDSIFGDPKLLTQYFVOENYLEYRQVPGSDPACYEFLWGP
ALietsYKVLHMHVKISGGPRISYPLLHEWALREGEE"
BASE COUNT      865 a 1050 c 1117 g 839 t
ORIGIN
Query Match     97.9%; Score 220.2; DB 9; Length 3871;
Best Local Similarity 98.7%; Pred. No. 6.7e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTTCTGTGATCTTCAGCAAGCTTCGGAATTCCTTGACGCTGGTCTTTGGCATC 60
|||
Db 2696 TACTTCTTTCTGTGATCTTCAGCAAGCTTCGGAATTCCTTGACGCTGGTCTTTGGCATC 2755
|||
QY 61 GAGCTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
|||
Db 2756 GAGCTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 2815
|||
QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGACAGGCTTCTTGATAATC 180
|||
Db 2816 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGACAGGCTTCTTGATAATC 2875
|||
QY 181 ATCTGGCCATAATCGCAAGAGAGGCGACTGTGCCCTTGAGGAG 225
|||
Db 2876 ATCTGGCCATAATCGCAAGAGAGGCGACTGTGCCCTTGAGGAG 2920
|||

RESULT 9
AF002997        245077 bp  DNA  linear  PRI 13-APR-2001
LOCUS           Homo sapiens chromosome X map Xq28, complete sequence.
DEFINITION      AF002997
ACCESSION       AF002997
VERSION         AF002997.2 GI:13621226
KEYWORDS        HTG; HTGS_ACTIVEFIN.
SOURCE          human.
ORGANISM        Homo sapiens
REFERENCE        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE           1 (bases 9444 to 72299)
                Gloeckner,G., Rosenthal,A., Drescher,B., Schattevoy,R., Poustka,A.
                and Kioschis,P.
                Genomic sequence in Xq28
                Unpublished
JOURNAL          2 (bases 1 to 245077)
REFERENCE        Galoczky,P., Schillhabel,M., Rosenthal,A. and Platzter,M.
AUTHORS          Chromosome X genomic sequence
TITLE           Unpublished
JOURNAL          3 (bases 1 to 245077)
REFERENCE        Gloeckner,G., Rosenthal,A., Drescher,B. and Schattevoy,R.
AUTHORS          Direct Submission
TITLE           Submitted (07-MAY-1997) Genome Analysis, Institute of Molecular
JOURNAL          Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
REFERENCE        4 (bases 1 to 245077)

```



```

nucleic acid sequences encoding them, used for the preparation of
fusion proteins and of compositions for vaccination
JOURNAL Patent: WO 9940188-A 6 12-AUG-1999;
SLAOUJI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)
FEATURES
    source          Location/Qualifiers
        ..1212
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /note="Melanoma tissue"
BASE COUNT      289 a   319 c   344 g   260 t
ORIGIN
Query Match      95.0%; Score 213.8; DB 6; Length 1212;
Best Local Similarity 96.9%; Pred. No. 2.2e+0;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1 TATTTCCTTCCGTGANTCCTCAGAAAGCTTCGGATTCCTTGACGTGCTTTGGGCATC 60
         |||
Db      673 TATTTCCTTCCGTGATCTTCAGAAAGCTTCCAGTTCCTTGACGTGCTTTGGGCATC 732

Qy      61 GAGCGTAGGAAGTGGACCCCATCGGCCAGCGTGATCATCTTTGCCACACTGCCTGGGCCTC 120
         |||
Db      733 GAGCGTAGGAAGTGGACCCCATCGGCCACTGTGTACATCTTTGCCACCTGCCTGGGCCTC 792

Qy      121 TCCTPACGATGCCCTGCTGGGTGACAATCAGATCATGCCACAGGACAGGCTTCCTGATAATC 180
         |||
Db      793 TCCPACGATGCCCTGCTGGGTGACAATCAGATCATGCCAAGGACGAGCCTCCTGATAATC 852

Qy      181 ATCTCGGCCATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 225
         |||
Db      853 GTCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 897

RESULT 11

```

[illegible]

LOCUS BC011744 1663 bp mRNA linear PRI 02-AUG-2001
 DEFINITION Homo sapiens, similar to melanoma antigen, family A, 3, clone
 ACCESSION MGC:19667 IMAGE:3345801, mRNA, complete cds.
 VERSION BC011744
 KEYWORDS BC011744.1 GI:15079897
 SOURCE MGC.
 ORGANISM homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1663)
 Strausberg R.
 Direct Submission
 Submitted (30-JUL-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, N.I., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
 Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
 Tionson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
 Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 27 Row: b Column: 12
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Similarity but not
 identity to protein.

FEATURES

Location/Qualifiers
 1..1663
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="MGC:19667 IMAGE:3345801"
 /tissue_type="Skin, melanotic melanoma."
 /clone_lib="NIH_MGC_20"
 /lab_host="DH10B-R"
 /note="Vector: pOTB7"
 145..1089
 /codon_start=1
 /product="Similar to melanoma antigen, family A, 3"
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 /translation="MPLEQRSQCKPEEGLEARGEALGLVGAQAPATERQEAASSST
 LVEVTGVEPAESDPPOSPOGASLPTTMVPLWSQSYEDSSNOEERGSTFPDPLE
 SEFOALSKVELVHFLLYKREPVTKAEMLSVGVNWQYFPFVIESKASSLQL
 VFGILEMVDPTGHLVIFATCLGSLDGLDGNQIMPKAGLLIIVLAIAREDCAPE
 EKIMELSVLEFVEDSILGDPKKLLTOHFQENYLEYRQVPGSDPACYEFLWGP
 ALVETSYVKVLHVMKISGGPHISYPPLHEWVLRGEE"
 411 a 398 c 448 g 406 t

CDS

BASE COUNT
 ORIGIN

Query Match 95.0%; Score 213.8; DB 9; Length 1663;
 Best Local Similarity 96.9%; Pred. No. 2.2e-40;
 Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 TATTTCCTTCCTGATCTTCAGCAAGCTCCGATCTCTTCAGCTGGCTTTGGCATC 60
 |||||||
 Db 577 TATTTCCTTCCTGATCTTCAGCAAGCTCCGATCTCTTCAGCTGGCTTTGGCATC 636

QY 61 GAGCTGATGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACTGCTGGGCTC 120
 |||||||
 Db 637 GAGCTGATGAAGTGGACCCCATCGGCCACTTGTACATCTTTGCCACTGCTGGGCTC 696
 |||||||
 QY 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCACGACAGGCTTCCTGATAATC 180
 |||||||
 Db 697 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCACGACAGGCTTCCTGATAATC 756
 |||||||
 QY 181 ATCCTGGCCATAATTCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
 |||||||
 Db 757 GTCCTGGCCATAATTCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 801
 |||||||

Search completed: September 4, 2002, 16:38:28
 Job time: 19506 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 14:29:00 ; Search time 114.14 seconds
(without alignments)
3384.491 Million cell updates/sec

Title: US-08-967-727-18

Perfect score: 225

Sequence: 1 TATTTCCTTCTGTGATCTT.....GCGACTGTGCCCTCAGGAG 225

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802.*

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2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
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24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | ID | Description |
|------------|-------|-------------|---------|-------------|
| 1 | 225 | 100.0 | 225 13 | AAQ32362 |
| 2 | 225 | 100.0 | 225 15 | AAQ72487 |
| 3 | 225 | 100.0 | 225 20 | AAQ84112 |
| 4 | 223.4 | 99.3 | 225 16 | AAQ84116 |
| 5 | 220.2 | 97.9 | 1362 20 | AAQ87596 |
| 6 | 220.2 | 97.9 | 1375 19 | AAQ22716 |
| 7 | 220.2 | 97.9 | 4204 22 | AAQ02056 |
| 8 | 213.8 | 95.0 | 666 22 | AAQ18141 |
| 9 | 213.8 | 95.0 | 945 22 | AAQ12993 |

| | | | | |
|----|-------|------|---------|-----------|
| 10 | 213.8 | 95.0 | 1212 20 | AAQ87592 |
| 11 | 213.8 | 95.0 | 1353 20 | AAQ87588 |
| 12 | 213.8 | 95.0 | 1640 15 | AAQ72480 |
| 13 | 213.8 | 95.0 | 1640 20 | AAQ84116 |
| 14 | 213.8 | 95.0 | 4204 20 | AAQ26974 |
| 15 | 213.8 | 95.0 | 4204 21 | AAQ37927 |
| 16 | 213.8 | 95.0 | 4204 22 | AAQ18140 |
| 17 | 212.2 | 94.3 | 1640 13 | AAQ32355 |
| 18 | 196.8 | 87.5 | 727 22 | AAQ21285 |
| 19 | 195.2 | 86.8 | 920 22 | ABA36364 |
| 20 | 195.2 | 86.8 | 920 22 | AAQ124300 |
| 21 | 195.2 | 86.8 | 920 22 | AAQ149576 |
| 22 | 195.2 | 86.8 | 1030 22 | AAQ21286 |
| 23 | 195.2 | 86.8 | 1956 22 | ABA26487 |
| 24 | 195.2 | 86.8 | 1956 22 | AAQ15118 |
| 25 | 195.2 | 86.8 | 1956 22 | AAQ136453 |
| 26 | 195.2 | 86.8 | 4157 13 | AAQ32353 |
| 27 | 195.2 | 86.8 | 4157 15 | AAQ72478 |
| 28 | 195.2 | 86.8 | 4157 20 | AAQ84114 |
| 29 | 195.2 | 86.8 | 4523 22 | AAQ06131 |
| 30 | 166 | 73.8 | 379 18 | AAQ63345 |
| 31 | 163.2 | 72.5 | 930 22 | AAQ12987 |
| 32 | 163.2 | 72.5 | 1084 15 | AAQ67866 |
| 33 | 163.2 | 72.5 | 1084 20 | AAQ08442 |
| 34 | 163.2 | 72.5 | 1094 15 | AAQ67865 |
| 35 | 163.2 | 72.5 | 1094 20 | AAQ08441 |
| 36 | 163.2 | 72.5 | 1338 20 | AAQ87593 |
| 37 | 163.2 | 72.5 | 1341 20 | AAQ87591 |
| 38 | 163.2 | 72.5 | 1624 22 | AAQ24676 |
| 39 | 163.2 | 72.5 | 1691 22 | AAQ69719 |
| 40 | 163.2 | 72.5 | 2418 20 | AAQ84103 |
| 41 | 163.2 | 72.5 | 2419 13 | AAQ32351 |
| 42 | 163.2 | 72.5 | 2419 15 | AAQ72476 |
| 43 | 163.2 | 72.5 | 2419 16 | AAQ05086 |
| 44 | 163.2 | 72.5 | 2419 20 | AAQ84112 |
| 45 | 163.2 | 72.5 | 2420 15 | AAQ72472 |

ALIGNMENTS

RESULT 1
AAQ32362
ID AAQ32362 standard; DNA; 225 BP.

AC AAQ32362;

XX 22-APR-1993 (first entry)

DE MAG-6 gene.

DE Melanoma antigen; MAG-6 gene.

KW Melanoma antigen; MAG-6 gene; melanoma antigen tumor rejection antigen;

XX tumor rejection antigen precursor; MAG-6 gene family; ss.

OS Homo sapiens.

XX WO9220356-A.

PD 26-NOV-1992.

PF 22-MAY-1992; 92WO-US04354.

PR 23-MAY-1991; 91US-0705702.

PR 09-JUL-1991; 91US-0728838.

PR 23-SEP-1991; 91US-0764364.

PR 12-DEC-1991; 91US-0807043.

XX (LUDW-) LUDWIG INST CANCER RES.

PI Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;

PI Van Den Eynde B, Van Der Bruggen P, Van Pel A;

XX WPI; 1992-415460/50.

XX Nucleic acid mol. encoding a human tumour rejection antigen
PT precursor - useful as an immunostimulant in a vaccine for
PT treating and preventing cancers, also useful in diagnosis
XX
XX
XX Disclosure; Page 88; 142pp; English.
XX
XX The sequences given in AAQ32352-69 represent a new family of genes
CC referred to as melanoma antigens (MAGE). The cDNAs of this gene
CC family were identified during the isolation of the antigen E gene.
CC The MAGE cDNAs, when tested, did not transfer expression of antigen
CC E, but they did show substantial homology to the antigen E cDNA
CC sequence. The MAGE DNAs share a certain degree of homology with each
CC other and are expressed in tumour cells including several types of
CC human tumor cells as well as in human tumors. MAGE expression is not
CC restricted to melanomas. MAGE refers to a family of tumor rejection
CC antigen precursors. The antigens resulting from these genes are
CC referred to as MAGE TRAs or melanoma antigen tumor rejection antigens.
CC See also AAQ32351.
XX
XX Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 13; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.6e-56;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCGAGCTGTCTTTGGCATC 60
Db 1 Tatttcttctgtgattcttcagcaaaagcttcgattcttcgtgagctgtctttggcatc 60
Qy 61 GAGCTGATGGAGTGGACCCCATCGGCGACGCTGTACATCTTTGGCACCTGCTGGGCCTC 120
Db 61 gagctgatggaagtggaccccatcgccacgtgtacatctttgccaacctgctgggacctc 120
Qy 121 TCCTACGATGGCCTGCTGGGTGACAAATCAGATCATGCCAGGACGCTTCTGTATATC 180
Db 121 tcctacgatggcctgctgggtgacaatcagatcatgcccaggacaggtctctgataatc 180
Qy 181 ATCTGGCCATAATCGCAAGAGGCGGACGTGTGCCCTGTAGAGGAG 225
Db 181 atcttgccataatcgcaagagggcgactgtgccccctgaggag 225

RESULT 2
AAQ72487
ID AAQ72487 standard; cDNA to mRNA; 225 BP.
XX
XX
XX AAQ72487;
XX
XX 22-JUN-1995 (first entry)
XX Tumour rejection antigen MAGE-6 cDNA.
XX
XX Tumour rejection antigen; melanoma antigen-6; MAGE-6; MAGE-3;
KW cancer; cytolytic T cells; antigen D; human leucocyte antigen;
KW ss.
XX
XX Homo sapiens.
XX
XX W09423031-A.
XX
XX 13-OCT-1994.
XX
XX 17-MAR-1994; 94WO-US02877.
XX
XX 26-MAR-1993; 93US-0037230.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
XX WPI; 1994-333192/41.

XX New tumour rejection antigen precursor MAGE3 - useful in
PT treatment and diagnosis of cancer
XX
XX Example 32; Page 73; 105pp; English.
XX
XX AAQ72487 is the cDNA sequence which codes for melanoma antigen-6
CC (MAGE-6). Another melanoma antigen MAGE-3 is encoded by
CC AAQ72470, this is a tumour rejection antigen precursor. Melanomas
CC characterised by the expression of MAGE-3 can be detected, or
CC monitored, by contacting a test sample with an agent that can
CC recognise MAGE-3. The melanoma can be treated by the administration
CC of cytolytic T cells specific for the complex of antigen D (the
CC mature rejection antigen derived from MAGE-3) and a human leucocyte
CC antigen (esp. HLA-A1).
XX
XX Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 15; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.6e-56;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCGAGCTGTCTTTGGCATC 60
Db 1 Tatttcttctgtgattcttcagcaaaagcttcgattcttcgtgagctgtctttggcatc 60
Qy 61 GAGCTGATGGAGTGGACCCCATCGGCGACGCTGTACATCTTTGGCACCTGCTGGGCCTC 120
Db 61 gagctgatggaagtggaccccatcgccacgtgtacatctttgccaacctgctgggacctc 120
Qy 121 TCCTACGATGGCCTGCTGGGTGACAAATCAGATCATGCCAGGACGCTTCTGTATATC 180
Db 121 tcctacgatggcctgctgggtgacaatcagatcatgcccaggacaggtctctgataatc 180
Qy 181 ATCTGGCCATAATCGCAAGAGGCGGACGTGTGCCCTGTAGAGGAG 225
Db 181 atcttgccataatcgcaagagggcgactgtgccccctgaggag 225

RESULT 3
AAQ84122
ID AAQ84122 standard; cDNA; 225 BP.
XX
XX
XX AC
XX
XX 08-SEP-1999 (first entry)
XX
XX MAGE-6 gene.
XX
XX Tumour rejection antigen; vaccine; cancer; MAGE-6 gene; ss.
XX
XX Homo sapiens.
XX
XX US5925729-A.
XX
XX 20-JUL-1999.
XX
XX 02-MAY-1994; 94US-0142368.
XX
XX 02-MAY-1994; 94US-0142368.
XX
XX 23-MAY-1991; 91US-0705702.
XX
XX 09-JUL-1991; 91US-0728838.
XX
XX 23-SEP-1991; 91US-0764365.
XX
XX 12-DEC-1991; 91US-0807043.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI Van Den Eynde B, Van Der Bruggen P, Van Pel A;
XX
XX WPI; 1999-418294/35.

PT New tumour rejection antigen is useful as a vaccine against
PT cancerous diseases
XX
PS Disclosure; Column 69-70; 58pp; English.
XX
CC This sequence represents the MAGE-6 gene sequence.
CC The invention relates to a tumour rejection antigen sequence that is
CC useful as a tumour rejection antigen for vaccination against cancerous
CC conditions.
XX
SQ Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 20; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.6e-56;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATTTCCTTCCTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATC 60
DB 1 tatttcttcttgatcttcagcaagcttcggattcttcgagctggtctcttggcattc 60
QY 61 GAGCTGATGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCGCTGGGCGCTC 120
DB 61 gagctgatggaagtggaccccatcgccacgtgtacatctttgcccacctgcttgggacctc 120
QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGACAGGCTTCCTGTGATAATC 180
DB 121 tctacgatggcctgctgggtgacaaatcagatcatgccagacaggcttctctgataatc 180
QY 181 ATCCCTGGCCATATTCGCAAGAGGGCGACTGTGCCCTGAGGAG 225
DB 181 atctctggccataatcgcaagagggcgactgtgccctgaggag 225

RESULT 4
ART01166
ID AAT01166 standard; DNA; 225 BP.
XX
AC AAT01166;
XX
DT 26-FEB-1996 (first entry)
DE MAGE-6 gene.
XX
KW MAGE-6; melanoma; tumour rejection antigen; cancer; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9523874-A1.
XX
PD 08-SEP-1995.
XX
PF 23-FEB-1995; 95WO-US02203.
XX
PR 30-NOV-1994; 94US-0346774.
PR 01-MAR-1994; 94US-0204727.
PR 10-MAR-1994; 94US-0209172.
PR 01-SEP-1994; 94US-0299849.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, Brasseur F, Chomez P, De Plaen E;
PI De Smet C, Gaugler B, Lethe B, Marchand M, Patard J;
PI Szikora J, Van Den Eynde B, Van Derbruggen P, Weynants P;
XX
WPI; 1995-320586/41.
XX
Determn. of cancerous condition(s) - using a nucleic acid as a
PT primer to determine expression of a MAGE tumour rejection antigen
PT precursor
XX
Example 32; Page 80; 121pp; English.

CC A family of human tumour rejection antigen precursor, MAGE, genes
CC (AAT05091-99, AAT01165-71) was isolated from various tumour cell lines.
CC cDNA (AAT01166) coding for MAGE-6 was obtd. from human melanoma
CC LB-33-MEL cells. MAGE serve as markers for tumour diagnosis. The
CC genes are silent in normal cells.
XX
SQ Sequence 225 BP; 44 A; 66 C; 57 G; 58 T; 0 other;

Query Match 99.3%; Score 223.4; DB 16; Length 225;
Best Local Similarity 99.6%; Pred. No. 1.9e-55;
Matches 224; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TATTTCCTTCCTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATC 60
DB 1 tatttcttcttgatcttcagcaagcttcggattcttcgagctggtctcttggcattc 60
QY 61 GAGCTGATGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCGCTGGGCGCTC 120
DB 61 gagctgatggaagtggaccccatcgccacgtgtacatctttgcccacctgcttgggacctc 120
QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGACAGGCTTCCTGTGATAATC 180
DB 121 tctacgatggcctgctgggtgacaaatcagatcatgccagacaggcttctctgataatc 180
QY 181 ATCCCTGGCCATATTCGCAAGAGGGCGACTGTGCCCTGAGGAG 225
DB 181 atctctggccataatcgcaagagggcgactgtgccctgaggag 225

RESULT 5
AAX87596
ID AAX87596 standard; cDNA; 1362 BP.
XX
AC AAX87596;
XX
DT 26-OCT-1999 (first entry)
DE CLYTA-MAGE-3-His fusion DNA.
XX
KW MAGE-3; CLYTA-MAGE-3-His; fusion protein; tumour; melanoma;
KW breast cancer; bladder cancer; lung cancer; colon cancer;
KW head and squamous cell carcinoma; oesophagus carcinoma; vaccine;
KW human; ss.
XX
OS Chimeric - Streptococcus pneumoniae.
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX
PN WO9940188-A2.
XX
PD 12-AUG-1999.
XX
PF 02-FEB-1999; 99WO-EP00660.
XX
PR 06-FEB-1998; 98GB-0002650.
PR 05-FEB-1998; 98GB-0002543.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
XX
WPI; 1999-494293/41.
DR P-PSDB; AAY06593.
XX
PT New protein derivatives used in cancer vaccine therapy for treating
PT a range of cancers including melanomas, carcinomas and cancers of
PT breast
XX
Example 10; Page 72; 72pp; English.
XX
This DNA sequence codes for a fusion protein (see AAY06593) composed
CC of the C-terminal portion of the Streptococcus pneumoniae LYTA


```
FT CDS      1..945
FT          /*tag= a
FT          /product= "MAGE-A3 protein"
XX
XX PN       WO200153833-A1.
XX PD       26-JUL-2001.
XX PF       19-JAN-2001; 2001WO-US02008.
XX PR       20-JAN-2000; 2000US-0177242.
XX PR       25-OCT-2000; 2000US-0243212.
XX PA       (LUDW-) LUDWIG INST CANCER RES.
XX
XX PI       Luiten R, Boon-Falleur T, Van Der Bruggen P, Stroobant V;
XX PI       Demotte N, Schultz E;
XX DR       WPI; 2001-488724/53.
XX DR       P-PSDB; AAE06853.
XX
XX PT       Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or
XX PT       HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used
XX PT       in diagnosis and treatment of a disorder characterized by expression of
XX PT       MAGE-A1 or -A3.
XX
XX PS       Example 3; Page 94-95; 103pp; English.
XX
XX CC       The invention relates to functional variants and isolated mimetics of a
XX CC       MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide,
XX CC       or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described
XX CC       in the specification. MAGE genes encode tumour rejection antigens
XX CC       (TRAS) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules.
XX CC       The MAGE antigenic peptide acts by binding to HLA molecules
XX CC       on tumour cells and stimulating recognition of these cells and thus
XX CC       signalling them to the immune system for destruction. The peptide when
XX CC       presented by HLA molecule induces the activation and stimulation of
XX CC       CD8+ cytotoxic T lymphocytes. The MAGE antigenic peptide is used to
XX CC       treat and diagnose disorders characterised by expression of MAGE-A1
XX CC       or -A3. Disorders include cancers e.g melanomas, oesophageal, lung,
XX CC       head and neck, breast, colorectal, prostate, renal, bladder,
XX CC       hepatocellular, papillary thyroid and gastric carcinomas, myelomas,
XX CC       brain tumours, sarcomas, seminomas, and ovarian tumours. The present
XX CC       sequence is human MAGE-A3 DNA.
XX
XX SQ       Sequence 945 BP; 210 A; 254 C; 278 G; 203 T; 0 other;

Query Match      95.0%; Score 213.8; DB 22; Length 945;
Best Local Similarity 96.9%; Pred. No. 1.8e-52;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTCTTTCCTGATCTTCAGCAAGCTTCAGATTCCTTCAGCTGCTTTGGCATC 60
   |||||||
DB 433 tattcttccctggtatcttcagcaagcttcagttccttcagctgtgtcttggcatc 492
   |||||||
QY 61 GAGCTGATGGAAGTGGACCCCATCGCCACGTGTACATCTTTGCCACCTGCTGGGCCCTC 120
   |||||||
DB 493 gagctgatggaagtggaccccatcgccactgtacatcttggccactgctgggacctc 552
   |||||||
QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGACAGGCTTCTGTATATC 180
   |||||||
DB 553 tctacgatggctgctgggtgacatcagatcatgcccaaggcctcctgataatc 612
   |||||||
QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
   |||||||
DB 613 gtccctggccataatcgaagagagggcgactgtgccctgaggag 657

RESULT 10
AAx87592
ID AAX87592 standard; cDNA; 1212 BP.
XX
```

```
AC AAX87592;
XX
XX DT       26-OCT-1999 (first entry)
XX DE       Haemagglutinin-MAGE-3-His fusion DNA.
XX
XX KW       MAGE-3; haemagglutinin; NSI-MAGE-3-His; fusion protein; tumour;
XX KW       melanoma; breast cancer; bladder cancer; lung cancer;
XX KW       head and squamous cell carcinoma; colon cancer;
XX KW       oesophagus carcinoma; vaccine; human; ss.
XX
XX OS       Chimeric - Influenza virus.
XX OS       Chimeric - Homo sapiens.
XX OS       Chimeric - synthetic.
XX
XX PN       WO9940188-A2.
XX PD       12-AUG-1999.
XX
XX PF       02-FEB-1999; 99WO-EP00660.
XX
XX PR       06-FEB-1998; 98GB-0002650.
XX PR       05-FEB-1998; 98GB-0002543.
XX
XX PA       (SMIK ) SMITHKLINE BECHAM BIOLOGICALS.
XX
XX PI       Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
XX
XX DR       WPI; 1999-494293/41.
XX DR       P-PSDB; AAY06591.
XX
XX PT       New protein derivatives used in cancer vaccine therapy for treating
XX PT       a range of cancers including melanomas, carcinomas and cancers of
XX PT       breast
XX
XX PS       Example 7; Page 69; 72pp; English.
XX
XX CC       This DNA sequence codes for a fusion protein (see AAY06591) composed
XX CC       of haemagglutinin NSI of influenza virus, the human MAGE-3
XX CC       tumour-associated antigen and a hexahistidine tail. A vector
XX CC       designed for recombinant expression of the fusion protein is
XX CC       provided. MAGE-3 cDNA was amplified using primers that altered the
XX CC       first 5 codons to Escherichia coli codon usage. The NSI moiety
XX CC       provided the fusion protein with additional exogenous T-helper
XX CC       epitopes. The invention relates to MAGE proteins fused to an
XX CC       immunological fusion partner, e.g. NSI-MAGE-3-His. These novel
XX CC       fusion proteins provide vaccines for immunotherapy of melanomas or
XX CC       other MAGE-associated tumours like breast, bladder, lung and
XX CC       non-small cell lung cancer, head and squamous cell carcinoma, colon
XX CC       carcinoma and oesophagus carcinoma.
XX
XX SQ       Sequence 1212 BP; 289 A; 319 C; 344 G; 260 T; 0 other;

Query Match      95.0%; Score 213.8; DB 20; Length 1212;
Best Local Similarity 96.9%; Pred. No. 2e-52;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTCTTTCCTGATCTTCAGCAAGCTTCAGATTCCTTCAGCTGCTTTGGCATC 60
   |||||||
DB 673 tattcttctctgtgattcagcaagcttcagttccttcagctgtgtcttggcatc 732
   |||||||
QY 61 GAGCTGATGGAAGTGGACCCCATCGCCACGTGTACATCTTTGGCACCTGCTGGGCCCTC 120
   |||||||
DB 733 gagctgatggaagtggaccccatcgccactgtacatcttggccactgctgggacctc 792
   |||||||
QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGACAGGCTTCTGTATATC 180
   |||||||
DB 793 tctacgatggctgctgggtgacatcagatcatgcccaaggcctcctgataatc 852
   |||||||
QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
   |||||||
DB 853 gtccctggccataatcgaagagagggcgactgtgccctgaggag 897
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QY 121 TCCTACGATGGCTGCTGGTGACAAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180
|||||
Db 3017 tctacgatggctgctgggtgacaatcagatcatgccccaggcaggccctcctgataatc 3076
|||||
QY 181 ATCTGCGCCATAATCGCAAGAGAGGGGAGCTGTGCCCTGAGGAG 225
|||||
Db 3077 gtcttgccataataatcgcaagagagggcgactgtgccctgagag 3121
|||||

RESULT 15
AAA37927
ID AAA37927 standard; cDNA; 4204 BP.
XX
AC AAA37927;
XX
DT 18-AUG-2000 (first entry)
DE Human MAGE-A3 nucleotide sequence.
XX
KW MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;
KW cancer; human; tumour; tumour associated gene product; ss.
XX
OS Homo sapiens.
XX
PN WO200020581-A1.
XX
PD 13-APR-2000.
XX
PF 15-SEP-1999; 99WO-US21230.
XX
PR 05-OCT-1998; 98US-0166448.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYVR-) UNIV VRIJE BRUSSEL.
XX
PI Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;
PI Schultz ES, Van Snick J, Lethe B, Thielemans K, Corthals J;
PI Heirman C;
XX
DR WPI; 2000-317713/27.
DR P-PSDB; AAB02565.
XX
PT New MAGE-A3 class II binding peptides, useful to diagnose and treat
PT tumours, are fragments of MAGE-A3 which bind to and are presented to T
PT lymphocytes by human leukocyte antigen class II molecules -
XX
PS Example 6; Page 96-98; 119pp; English.
XX
CC The present invention relates to MAGE-A3 (tumour associated gene
CC product) human leukocyte antigen (HLA) class II-binding peptides (see
CC AAB02566-B02595, and AAB02633-B02637). These peptides are presented to T
CC cells in the context of HLA class II molecules. The peptides stimulate
CC the activity and proliferation of CD4+ T lymphocytes. The invention also
CC includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928
CC and AAA37938-A37940). The peptides and nucleotide sequences can be used
CC to create antibodies against the MAGE-A3 peptides, the antibodies,
CC peptides and nucleotide sequences can be used to create a vaccine. The
CC expression of MAGE-3, particularly cancer. The methods can also be used
CC in the diagnosis of disorders associated with MAGE-3 expression. Included
CC in the invention are other human tumour antigens (see AAB02596-B02637),
CC and PCR primers used in the course of the invention (see AAA37929-A37937
CC and AAA37941-A37942).
XX
SQ Sequence 4204 BP; 944 A; 1144 C; 1223 G; 893 T; 0 other;
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Query Match 95.0%; Score 213.8; DB 21; Length 4204;
Best Local Similarity 96.9%; Pred. No. 2.8e-52;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCCTTCCTGATCTTCAGCAAGCTTCGGATTCCTTCGACGTGGTCTTTGGCATC 60
|||||

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Db 2897 tattttcttctgtgatctttcagcaaaagcttccagttccttgcagctgggtctttggcgc 2956
QY 61 GAGCTGATGAAGTGGACCCCATCGGCCAGTGTTACATCTTCCACACCTGCCTGGGCTC 120
|||||
Db 2957 gagctgatggaaagtggaccatcgccactgtacatctttgccacctgctgggctc 3016
|||||
QY 121 TCCTACGATGGCTGCTGGTGACAAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180
|||||
Db 3017 tctacgatggcctgctgggtgacaatcagatcatgccccaggcaggccctcctgataatc 3076
|||||
QY 181 ATCTGCGCCATAATCGCAAGAGAGGGGAGCTGTGCCCTGAGGAG 225
|||||
Db 3077 gtcttgccataataatcgcaagagagggcgactgtgccctgagag 3121
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Search completed: September 4, 2002, 20:16:17
Job time: 20837 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 15:38:10 ; Search time 62.69 seconds
(without alignments)
881.601 Million cell updates/sec

Title: US-08-967-727-18

Perfect score: 225

Sequence: 1 TATTTCCTTCCTGATCTT.....GCCACTGTGCCCTGAGGAG 225

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 225 | 100.0 | 225 | 1 | US-07-807-043B-15 |
| 2 | 225 | 100.0 | 225 | 1 | US-08-299-849B-18 |
| 3 | 225 | 100.0 | 225 | 1 | US-08-142-368A-18 |
| 4 | 225 | 100.0 | 225 | 3 | US-08-967-727-18 |
| 5 | 225 | 100.0 | 225 | 4 | US-08-037-230D-18 |
| 6 | 220.2 | 97.9 | 945 | 4 | US-09-056-105-7 |
| 7 | 220.2 | 97.9 | 1019 | 4 | US-09-056-105-13 |
| 8 | 220.2 | 97.9 | 1375 | 2 | US-08-993-738A-2 |
| 9 | 220.2 | 97.9 | 1375 | 4 | US-08-713-354C-2 |
| 10 | 213.8 | 95.0 | 1640 | 1 | US-07-807-043B-11 |
| 11 | 213.8 | 95.0 | 1640 | 1 | US-08-299-849B-11 |
| 12 | 213.8 | 95.0 | 1640 | 2 | US-08-142-368A-11 |
| 13 | 213.8 | 95.0 | 1640 | 3 | US-08-967-727-11 |
| 14 | 213.8 | 95.0 | 1640 | 4 | US-08-037-230D-11 |
| 15 | 213.8 | 95.0 | 4204 | 2 | US-08-928-615-1 |
| 16 | 213.8 | 95.0 | 4204 | 4 | US-09-056-105-6 |
| 17 | 213.8 | 95.0 | 4204 | 4 | US-09-166-448-1 |
| 18 | 195.2 | 86.8 | 4157 | 1 | US-07-807-043B-9 |
| 19 | 195.2 | 86.8 | 4157 | 1 | US-08-299-849B-9 |
| 20 | 195.2 | 86.8 | 4157 | 2 | US-08-142-368A-9 |
| 21 | 195.2 | 86.8 | 4157 | 3 | US-08-967-727-9 |
| 22 | 195.2 | 86.8 | 4157 | 4 | US-08-037-230D-9 |
| 23 | 195.2 | 86.8 | 4559 | 4 | US-09-056-105-5 |
| 24 | 163.2 | 72.5 | 1084 | 2 | US-08-184-009-110 |
| 25 | 163.2 | 72.5 | 1084 | 2 | US-08-458-356-110 |
| 26 | 163.2 | 72.5 | 1084 | 4 | US-08-460-736-110 |
| 27 | 163.2 | 72.5 | 1094 | 2 | US-08-184-009-109 |

Sequence 109, App
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ALIGNMENTS

RESULT 1

US-07-807-043B-15

; Sequence 15, Application US/07807043B

; Patent No. 5342774

; GENERAL INFORMATION:

; APPLICANT: Boon, Thierry, Van den Eynde, Beno t

; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor

; NUMBER OF INVENTIONS: Rejection Antigens and Uses Thereof

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/807,043B

; FILING DATE: 19911212

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/764,364

; FILING DATE: 23-SEPTEMBER-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/728,838

; FILING DATE: 9-JULY-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/705,702

; FILING DATE: 23-May-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 5342774man D.

; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: LUD 253.3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 225 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: singular

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

; FEATURE:

; NAME/KEY: MAGE-6 gene

; US-07-807-043B-15

Query Match 100.0%; Score 225; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCCTTCCTGTCATCTTCAGCAAAAGCTTCGGATTCTTCGACGCTGGTCTTTGGCATC 60
|||||
Db 1 TATTTCCTTCCTGTCATCTTCAGCAAAAGCTTCGGATTCTTCGACGCTGGTCTTTGGCATC 60
|||||

QY 61 GAGCTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
|||||
Db 61 GAGCTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
|||||

QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGACAGGCTTCCTGTATAATC 180
|||||
Db 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGACAGGCTTCCTGTATAATC 180
|||||

QY 181 ATCTGGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG 225
|||||
Db 181 ATCTGGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG 225
|||||

RESULT 2

US-08-299-849B-18
; Sequence 18, Application US/08299849B
; Patent No. 5612201
; GENERAL INFORMATION:
; APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
; APPLICANT: Leth, Bernard; Srikora, Jean-Pierre; De Smet, Charles;
; APPLICANT: Chomez, Patrick
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,849B
; FILING DATE: 1-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5612201man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5355
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: MAGE-6 gene
US-08-299-849B-18

Query Match 100.0%; Score 225; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCCTTCCTGTCATCTTCAGCAAAAGCTTCGGATTCTTCGACGCTGGTCTTTGGCATC 60
|||||
Db 1 TATTTCCTTCCTGTCATCTTCAGCAAAAGCTTCGGATTCTTCGACGCTGGTCTTTGGCATC 60
|||||

QY 61 GAGCTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
|||||
Db 61 GAGCTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
|||||

QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGACAGGCTTCCTGTATAATC 180
|||||
Db 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGACAGGCTTCCTGTATAATC 180
|||||

QY 181 ATCTGGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG 225
|||||
Db 181 ATCTGGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG 225
|||||

RESULT 3

US-08-142-368A-18
; Sequence 18, Application US/08142368A
; Patent No. 5925729
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
; APPLICANT: Van den Eynde, Beno t; Van pel, Aline; De Plaen, Etienne;
; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,368A
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5925729man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: MAGE-6 gene
US-08-142-368A-18

Query Match 100.0%; Score 225; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCCCTTGACGTGGTCTTTGGCATC 60
DB 1 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCCCTTGACGTGGTCTTTGGCATC 60
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
DB 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGGACAGCTTCCTGATAATC 180
DB 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGGACAGCTTCCTGATAATC 180
QY 181 ATCTGCGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
DB 181 ATCTGCGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225

RESULT 4
US-08-967-727-18
Sequence 18, Application US/0896727
Patent No. 6025474
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,727
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6025474man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: MAGE-6 gene
US-08-967-727-18

Query Match 100.0%; Score 225; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCCCTTGACGTGGTCTTTGGCATC 60
DB 1 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCCCTTGACGTGGTCTTTGGCATC 60
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
DB 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGGACAGCTTCCTGATAATC 180
DB 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGGACAGCTTCCTGATAATC 180
QY 181 ATCTGCGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
DB 181 ATCTGCGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225

RESULT 5
US-08-037-230D-18
Sequence 18, Application US/08037230D
Patent No. 6235525
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/037,230D
FILING DATE: 26-MARCH-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6235525man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: MAGE-6 gene
US-08-037-230D-18

Query Match 100.0%; Score 225; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCAATC 60
|||
Db 1 TATTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCAATC 60
|||

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACAGTGATACATCTTTGCCACCTGCTGGGCCTC 120
|||
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCACAGTGATACATCTTTGCCACCTGCTGGGCCTC 120
|||

Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATATGCCCCAGGACAGGCTTCTGTATAATC 180
|||
Db 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATATGCCCCAGGACAGGCTTCTGTATAATC 180
|||

Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG 225
|||
Db 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG 225
|||

RESULT 6
US-09-056-105-7
; Sequence 7, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-7

Query Match 97.9%; Score 220.2; DB 4; Length 945;
Best Local Similarity 98.7%; Pred. No. 2.6e-60;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TATTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCAATC 60
|||
Db 433 tacttttctgtgatcttcagcaaaagcttcogattccgattccttgagctggtctttggcatc 492
|||

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACAGTGATACATCTTTGCCACCTGCTGGGCCTC 120
|||
Db 493 gagctgatggaagtggaccccatcgccaagtgatcatctttgcaacctgctgggcctc 552
|||

Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATATGCCCCAGGACAGGCTTCTGTATAATC 180
|||
Db 553 tcctacgatggcctgctgggtgacaatcagatcatgccccaaagacaggtcttctgataatc 612
|||

Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG 225
|||
Db 613 atcctggccataatcgcaaaagaggcgactgtgccccctgaggag 657
|||

RESULT 7
US-09-056-105-13
; Sequence 13, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1019
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-13

Query Match 97.9%; Score 220.2; DB 4; Length 1019;
Best Local Similarity 98.7%; Pred. No. 2.7e-60;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TATTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCAATC 60
|||
Db 498 tacttttctgtgatcttcagcaaaagcttcogattccttgagctggtctttggcatc 557
|||

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACAGTGATACATCTTTGCCACCTGCTGGGCCTC 120
|||
Db 558 gagctgatggaagtggaccccatcgccaagtgatcatctttgcaacctgctgggcctc 617
|||

Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATATGCCCCAGGACAGGCTTCTGTATAATC 180
|||
Db 618 tcctacgatggcctgctgggtgacaatcagatcatgccccaaagacaggtcttctgataatc 677
|||

Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG 225
|||
Db 678 atcctggccataatcgcaaaagaggcgactgtgccccctgaggag 722
|||

RESULT 8
US-08-993-738A-2
; Sequence 2, Application US/08993738A
; Patent No. 5928938
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre; DePlaen Etienne;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Complex With
; TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,738A
; FILING DATE: 19-December-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,354
; FILING DATE: 13-September-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5928938man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5460.1 DIV - JEL/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1375 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-993-738A-2

Query Match 97.9%; Score 220.2; DB 2; Length 1375;
Best Local Similarity 98.7%; Pred. No. 3e-60;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TATTCTTTCTCTGTGATCTTCAGCAAGCTTCGGATTCTTCGAGCTGGTCTTTGGCATC 60
Db 592 TACTTCTTTCTCTGTGATCTTCAGCAAGCTTCGGATTCTTCGAGCTGGTCTTTGGCATC 651
QY 61 GAGCTGATGGAAGTGAGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 652 GAGCTGATGGAAGTGAGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 711
QY 121 TCCTACGATGGCTGTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 180
Db 712 TCCTACGATGGCTGTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 771
QY 181 ATCTGTGCCATAATCGCAAGAGGGGCGACTGTGCCCTGAGGAG 225
Db 772 ATCTGTGCCATAATCGCAAGAGGGGCGACTGTGCCCTGAGGAG 816

RESULT 9
US-08-713-354C-2
; Sequence 2, Application US/08713354C
; Patent No. 6265215
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre; DePlaen Etienne;

; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Complex With
; TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,354C
; FILING DATE: 13-September-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6265215man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5460
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1375 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-713-354C-2

Query Match 97.9%; Score 220.2; DB 4; Length 1375;
Best Local Similarity 98.7%; Pred. No. 3e-60;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TATTCTTTCTCTGTGATCTTCAGCAAGCTTCGGATTCTTCGAGCTGGTCTTTGGCATC 60
Db 592 TACTTCTTTCTCTGTGATCTTCAGCAAGCTTCGGATTCTTCGAGCTGGTCTTTGGCATC 651
QY 61 GAGCTGATGGAAGTGAGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 652 GAGCTGATGGAAGTGAGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 711
QY 121 TCCTACGATGGCTGTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 180
Db 712 TCCTACGATGGCTGTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 771
QY 181 ATCTGTGCCATAATCGCAAGAGGGGCGACTGTGCCCTGAGGAG 225
Db 772 ATCTGTGCCATAATCGCAAGAGGGGCGACTGTGCCCTGAGGAG 816

RESULT 10
US-07-807-043B-11
; Sequence 11, Application US/07807043B
; Patent No. 5342774
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry, Van den Eynde, Beno t
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,043B
FILING DATE: 19911212
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5342774man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 253.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: singular
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: cDNA MAGE-3
US-07-807-043B-11

Query Match 95.0%; Score 213.8; DB 1; Length 1640;
Best Local Similarity 96.9%; Pred. No. 3.4e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGTCTTTGGCATC 60
Db 604 TATTTCTTCTGTGATCTTCAGCAAGCTTCCAGTTCCTTGACGCTGGTCTTTGGCATC 663
Qy 61 GAGCTGATGGAAGTGGAGCCCATCGGCACGTGTACATCTTTGGCACCTGCTGGGCCTC 120
Db 664 GAGCTGATGGAAGTGGAGCCCATCGGCACCTGTGTACATCTTTGGCACCTGCTGGGCCTC 723
Qy 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGAGGCTTCTGTGATAATC 180
Db 724 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGAGGCTTCTGTGATAATC 783
Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGTAGGAG 225
Db 784 GTCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGTAGGAG 828

RESULT 11
US-08-299-849B-11
Sequence 11, Application US/08299849B
Patent No. 5612201
GENERAL INFORMATION:
APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
APPLICANT: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felie & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,849B
FILING DATE: 1-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5612201man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5355
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: cDNA MAGE-3
US-08-299-849B-11

Query Match 95.0%; Score 213.8; DB 1; Length 1640;
Best Local Similarity 96.9%; Pred. No. 3.4e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGTCTTTGGCATC 60
Db 604 TATTTCTTCTGTGATCTTCAGCAAGCTTCCAGTTCCTTGACGCTGGTCTTTGGCATC 663
Qy 61 GAGCTGATGGAAGTGGAGCCCATCGGCACGTGTACATCTTTGGCACCTGCTGGGCCTC 120
Db 664 GAGCTGATGGAAGTGGAGCCCATCGGCACCTGTGTACATCTTTGGCACCTGCTGGGCCTC 723
Qy 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGAGGCTTCTGTGATAATC 180
Db 724 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGAGGCTTCTGTGATAATC 783
Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGTAGGAG 225
Db 784 GTCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGTAGGAG 828

RESULT 12
US-08-142-368A-11
Sequence 11, Application US/08142368A
Patent No. 5925729
GENERAL INFORMATION:
APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;

APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De plaen, Etienne;
APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5925729man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
FEATURE:
NAME/KEY: cdna MAGE-3
US-08-142-368A-11

Query Match 95.0%; Score 213.8; DB 2; Length 1640;
Best Local Similarity 96.9%; Pred. No. 3.4e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TATTTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATC 60
Db 604 TATTTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATC 663
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACTCGCTGGGCCTC 120
Db 664 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACTCGCTGGGCCTC 723
QY 121 TCCTAGCATGGCCTGCTGGTGACAAATCAGATCATGCCAGGAGAGGCTTCCTGATAATC 180
Db 724 TCCTAGCATGGCCTGCTGGTGACAAATCAGATCATGCCAGGAGAGGCTTCCTGATAATC 783
QY 181 ATCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTCAGGAG 225
Db 784 GTCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTCAGGAG 828

RESULT 13
US-08-967-727-11
Sequence 11, Application US/08967727
Patent No. 6025474
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,727
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6025474man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
FEATURE:
NAME/KEY: cdna MAGE-3
US-08-967-727-11

Query Match 95.0%; Score 213.8; DB 3; Length 1640;
Best Local Similarity 96.9%; Pred. No. 3.4e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TATTTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATC 60
Db 604 TATTTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATC 663
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACTCGCTGGGCCTC 120

Db 664 GAGCTGATGGAAGTGGAGCCCATCGGCACCTGTACATCTTTGGCACCTGCTGGGCGTC 723
QY 121 TCCTACGATGCGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTCTGATAATC 180
Db 724 TCCTACGATGCGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTCTGATAATC 783
QY 181 ATCTGTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCCTGAGGAG 225
Db 784 GTCTGTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCCTGAGGAG 828

RESULT 14
US-08-037-230D-11
; Sequence 11, Application US/08037230D
; Patent No. 6235525
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/037,230D
; FILING DATE: 26-MARCH-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6235525man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1640 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mrna
; FEATURE:
; NAME/KEY: cdna MAGE-3
US-08-037-230D-11

Query Match 95.0%; Score 213.8; DB 4; Length 1640;
Best Local Similarity 96.9%; Pred. No. 3.4e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTTCTCTGTGATCTTTTCAGCAAAAGCTTCCGATTCCTTGACAGCTGGTCTTTGGCATC 60
Db 604 TATTTCTTTCTCTGTGATCTTTTCAGCAAAAGCTTCCAGTTTCTCTTGACAGCTGGTCTTTGGCATC 663
QY 61 GAGCTGATGGAAGTGGAGCCCATCGGCACCTGTACATCTTTGCCACCTGCCTGGGCGTC 120
Db 664 GAGCTGATGGAAGTGGAGCCCATCGGCACCTGTGTACATCTTTGCCACCTGCCTGGGCGTC 723
QY 121 TCCTACGATGCGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTCTGATAATC 180
Db 724 TCCTACGATGCGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTCTGATAATC 783
QY 181 ATCTGTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCCTGAGGAG 225
Db 784 GTCTGTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCCTGAGGAG 828

RESULT 15
US-08-928-615-1
; Sequence 1, Application US/08928615
; Patent No. 5965535
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED
; TITLE OF INVENTION: BY HLA CLASS II MOLECULES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,615
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4204 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 2465...3406
US-08-928-615-1

Query Match 95.0%; Score 213.8; DB 2; Length 4204;
Best Local Similarity 96.9%; Pred. No. 5e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TATTTCTTTCTCTGTGATCTTTTCAGCAAAAGCTTCCGATTCCTTGACAGCTGGTCTTTGGCATC 60

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|||||
Db 2897 TATTTCTTTCTCTGTATCTTCAGCAAGCTTCAGTTCCCTTGCAGCTGGTCTTTGGCATC 2956
QY 61 GAGCTGATGGAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGGCTGGGCTC 120
Db 2957 GAGCTGATGGAGTGGACCCCATCGGCCACCTTGTACATCTTTGCCACCTGGCTGGGCTC 3016
QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180
Db 3017 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 3076
QY 181 ATCCTGGCCATAATCGCAAGAGGGGACTGTGCCCCCTGAGGAG 225
Db 3077 GTCCCTGGCCATAATCGCAAGAGGGGACTGTGCCCCCTGAGGAG 3121
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Search completed: September 4, 2002, 21:15:19
Job time: 20229 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 10:40:10 ; Search time 1028.98 Seconds
(without alignments)
1660.387 Million cell updates/sec

Title: US-08-967-727-18

Perfect score: 225

Sequence: 1 TATTCTTCTCTGATCTT.....GCGACTGTGCCCTGAGGAG 225

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:.*
2: em_esthum:.*
3: em_estin:.*
4: em_estmu:.*
5: em_estov:.*
6: em_estpl:.*
7: em_estro:.*
8: em_htc:.*
9: gb_est1:.*
10: gb_est2:.*
11: gb_htc:.*
12: gb_gss:.*
13: em_gss_hum:.*
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15: em_gss_pln:.*
16: em_gss_vrt:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 220.2 | 97.9 | 563 | 10 | BG477228 |
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| 3 | 220.2 | 97.9 | 876 | 10 | BF792356 |
| 4 | 220.2 | 97.9 | 878 | 10 | BG397171 |
| 5 | 220.2 | 97.9 | 886 | 10 | BG476078 |
| 6 | 213.8 | 95.0 | 623 | 10 | BF793889 |
| 7 | 213.8 | 95.0 | 686 | 10 | BG575715 |
| 8 | 213.8 | 95.0 | 704 | 10 | BT090658 |
| 9 | 213.8 | 95.0 | 769 | 10 | BF765526 |
| 10 | 213.8 | 95.0 | 872 | 10 | BM449726 |
| 11 | 212.8 | 94.6 | 1021 | 10 | BM470991 |
| 12 | 202.6 | 90.0 | 934 | 10 | BG280738 |
| 13 | 201.4 | 89.5 | 795 | 10 | BE541476 |
| 14 | 197.6 | 87.8 | 803 | 10 | BM015882 |
| 15 | 196.8 | 87.5 | 590 | 10 | BE897495 |
| 16 | 196.8 | 87.5 | 680 | 10 | BE563063 |
| 17 | 196.4 | 87.3 | 768 | 10 | BI086876 |

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| 18 | 196 | 87.1 | 767 | 10 | BI092532 |
| 19 | 195.8 | 87.0 | 1114 | 10 | BM479202 |
| 20 | 195.2 | 86.8 | 1089 | 10 | BG029985 |
| 21 | 194.8 | 86.6 | 809 | 10 | BI855745 |
| 22 | 194 | 86.2 | 707 | 10 | BG760839 |
| 23 | 193.6 | 86.0 | 484 | 10 | BF970108 |
| 24 | 193.6 | 86.0 | 784 | 10 | BF793468 |
| 25 | 178.8 | 79.5 | 845 | 10 | BG481937 |
| 26 | 176.8 | 78.6 | 894 | 10 | BG765817 |
| 27 | 165.4 | 73.5 | 810 | 9 | AL526639 |
| 28 | 164.6 | 73.2 | 816 | 10 | BI086919 |
| 29 | 163.4 | 72.6 | 797 | 10 | BI087493 |
| 30 | 162.8 | 72.4 | 929 | 10 | BE896896 |
| 31 | 159.6 | 70.9 | 962 | 10 | BG116297 |
| 32 | 159.6 | 70.9 | 1050 | 10 | BG024106 |
| 33 | 156.4 | 69.5 | 956 | 10 | BE900736 |
| 34 | 154.8 | 68.8 | 876 | 10 | BE795782 |
| 35 | 153.2 | 68.1 | 929 | 10 | BE275276 |
| 36 | 152.8 | 67.9 | 704 | 10 | BG764972 |
| 37 | 150.2 | 66.8 | 845 | 10 | BI089076 |
| 38 | 148.8 | 66.1 | 716 | 10 | BM015975 |
| 39 | 147.6 | 65.6 | 922 | 10 | BG115115 |
| 40 | 147.6 | 65.6 | 946 | 10 | BF983819 |
| 41 | 146 | 64.9 | 948 | 9 | AL562721 |
| 42 | 143.4 | 63.7 | 941 | 10 | BI830314 |
| 43 | 141.8 | 63.0 | 820 | 10 | BG481340 |
| 44 | 138.6 | 61.6 | 1109 | 10 | BG333682 |
| 45 | 138.2 | 61.4 | 597 | 10 | BE281072 |

ALIGNMENTS

RESULT 1

BG477228

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG477228 563 bp mRNA linear EST 21-MAR-2001
60252437F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4642641 5',
mRNA sequence.
BG477228
BG477228.1 GI:13409507
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 563)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW411 row: i column: 10
High quality sequence stop: 499.
Location/Qualifiers
1. .563
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4642641"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site: 1; XhoI: Site_2;
EcoRI: CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(s). Size-selected >500bp for average
Insert size 1.8kb. Library constructed by Ling Hong in

FEATURES
source

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT
ORIGIN

Query Match 97.9%; Score 220.2; DB 10; Length 563;
Best Local Similarity 98.7%; Pred. No. 3.5e-48;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTTCTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
|||
Db 191 TACTCTTTCTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 250
|||
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTTGCACCTGCTGGGCTC 120
|||
Db 251 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTTGCACCTGCTGGGCTC 310
|||
QY 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCCTGATAATC 180
|||
Db 311 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCCTGATAATC 370
|||

QY 181 ATCTCTGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
|||||

Db 371 ATCTCTGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 415
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RESULT 2

LOCUS BG476912 776 bp mRNA linear EST 21-MAR-2001
DEFINITION 602524881F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4642868 5',
mRNA sequence.

ACCESSION BG476912

VERSION BG476912.1

GI:13409178

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 776)

Authors Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Title Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Journal NIH-MGC http://mgi.nci.nih.gov/.

Comment Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTF

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Plate: L1CM1412 row: b column: 21

High quality sequence stop: 747.

Location/Qualifiers

1..776

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4642868"

/clone_lib="NIH_MGC_20"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/note="organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; CDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCAGGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 180 a 197 c 232 g 167 t

ORIGIN

Query Match 97.9%; Score 220.2; DB 10; Length 776;
Best Local Similarity 98.7%; Pred. No. 3.8e-48;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTTCTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
|||
Db 191 TACTCTTTCTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 250
|||
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTTGCACCTGCTGGGCTC 120
|||
Db 251 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTTGCACCTGCTGGGCTC 310
|||
QY 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCCTGATAATC 180
|||
Db 311 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCCTGATAATC 370
|||

QY 181 ATCTCTGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
|||||

Db 371 ATCTCTGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 415
|||||

RESULT 3

LOCUS BF792356 876 bp mRNA linear EST 12-JAN-2001
DEFINITION 60252896F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4345222 5',
mRNA sequence.

ACCESSION BF792356

VERSION BF792356.1

GI:12097410

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 876)

Authors Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Title Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Journal NIH-MGC http://mgi.nci.nih.gov/.

Comment Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Plate: L1AM9964 row: p column: 23

High quality sequence stop: 780.

Location/Qualifiers

1..876

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4345222"

/clone_lib="NIH_MGC_84"

/tissue_type="adrenal cortex carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:

NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT

primed. Average insert size 1.229 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."

BASE COUNT 185 a 215 c 248 g 228 t

ORIGIN

Query Match 97.9%; Score 220.2; DB 10; Length 876;
Best Local Similarity 98.7%; Pred. No. 3.9e-48;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTTCTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
|||

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Db 78 TATTTCCTTCCTGTGATCTTCATCAAGCTTCGGATTCCCTGCGTGGTCTTTGGCATC 137
QY 61 GAGCTGATGAAGTGACCCCATCGGCCACGCTGATACATCTTTGCCACCTGCGCTGGGCCCTC 120
Db 138 GAGCTGATGAAGTGACCCCATCGGCCACGCTGATACATCTTTGCCACCTGCGCTGGGCCCTC 197
QY 121 TCCTAGATGGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 180
Db 198 TCCTAGATGGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 257
QY 181 ATCCCTGGCCATAATCCAGAGAGGCGGACTGTGCCCTGAGGAG 225
Db 258 ATCCCTGGCCATAATCCAGAGAGGCGGACTGTGCCCTGAGGAG 302

RESULT 4
BG397171
LOCUS BG397171 878 bp mRNA linear EST 12-MAR-2001
DEFINITION 602434130F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4552086 5',
mRNA sequence.
ACCESSION BG397171
VERSION BG397171.1 GI:13290619
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 878)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1247 row: 1 column: 07
High quality sequence stop: 866.
FEATURES
Location/Qualifiers
1..878
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4552086"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```
BASE COUNT 197 a 214 c 262 g 205 t
ORIGIN
Query Match 97.9%; Score 220.2; DB 10; Length 878;
Best Local Similarity 98.7%; Pred. No. 3.9e-48;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTTCCTTCCTGTGATCTTCAGAAAGCTTCGGATTCCCTGCGTGGTCTTTGGCATC 60
Db 190 TACTTCTTCCTGTGATCTTCAGAAAGCTTCGGATTCCCTGCGTGGTCTTTGGCATC 249
QY 61 GAGCTGATGAAGTGACCCCATCGGCCACGCTGATACATCTTTGCCACCTGCGCTGGGCCCTC 120
Db 250 GAGCTGATGAAGTGACCCCATCGGCCACGCTGATACATCTTTGCCACCTGCGCTGGGCCCTC 309
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QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 180
Db 310 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 369
QY 181 ATCCTGGCCATAATCCAGAGAGGCGGACTGTGCCCTGAGGAG 225
Db 370 ATCCTGGCCATAATCCAGAGAGGCGGACTGTGCCCTGAGGAG 414

RESULT 5
BG476078
LOCUS BG476078 886 bp mRNA linear EST 21-MAR-2001
DEFINITION 602520963F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4639670 5',
mRNA sequence.
ACCESSION BG476078
VERSION BG476078.1 GI:13408357
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 886)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1403 row: m column: 15
High quality sequence stop: 730.
FEATURES
Location/Qualifiers
1..886
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4639670"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```
BASE COUNT 183 a 231 c 262 g 210 t
ORIGIN
Query Match 97.9%; Score 220.2; DB 10; Length 886;
Best Local Similarity 98.7%; Pred. No. 3.9e-48;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTTCCTTCCTGTGATCTTCAGAAAGCTTCGGATTCCCTGCGTGGTCTTTGGCATC 60
Db 94 TACTTCTTCCTGTGATCTTCAGAAAGCTTCGGATTCCCTGCGTGGTCTTTGGCATC 153
QY 61 GAGCTGATGAAGTGACCCCATCGGCCACGCTGATACATCTTTGCCACCTGCGCTGGGCCCTC 120
Db 154 GAGCTGATGAAGTGACCCCATCGGCCACGCTGATACATCTTTGCCACCTGCGCTGGGCCCTC 213
QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 180
Db 214 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 273
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Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
|||||
Db 274 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 318
|||||

RESULT 6
BF793889
LOCUS 60225285f1 NIH_MGC_84 623 bp mRNA linear EST 12-JAN-2001
DEFINITION 60225285f1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4347380 5',
mRNA sequence.
ACCESSION BF793889
VERSION BF793889.1 GI:12098943
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 623)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9970 row: j column: 21
High quality sequence stop: 622.
Location/Qualifiers
1. .623
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4347380"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
Noti; Site_2: SalI; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 136 a 173 c 177 g 137 t
ORIGIN

Query Match 95.0%; Score 213.8; DB 10; Length 623;
Best Local Similarity 96.9%; Pred. No. 1.8e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATCTTGTGACGTGGTCTTTGGCATC 60
|||||
Db 326 TATTTCTTCTGTGATCTTCAGCAAGCTTCCAGTCTTGTGACGTGGTCTTTGGCATC 385
|||||

Qy 61 GAGCTGATGGAAGTGGACCCCATCGCCACGTGTACATCTTTGGCACCTGCTGGGCCTC 120
|||||
Db 386 GAGCTGATGGAAGTGGACCCCATCGCCACGTGTACATCTTTGGCACCTGCTGGGCCTC 445
|||||

Qy 121 TCCTACGATGGCTGCTGGTGACAAATCAGATCATGCCACAGGACAGGCTTCTGTATAATC 180
|||||
Db 446 TCCTACGATGGCTGCTGGTGACAAATCAGATCATGCCACAGGACAGGCTTCTGTATAATC 505
|||||

Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
|||||
Db 506 GTCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 550
|||||

RESULT 7
BG575715
LOCUS 602853894f1 NIH_MGC_10 704 bp mRNA linear EST 20-JUN-2001
DEFINITION 602853894f1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:495238 5',
mRNA sequence.
ACCESSION BI090658
VERSION BI090658.1 GI:14508988
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 704)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM11018 row: 1 column: 23
High quality sequence stop: 703.
FEATURES
Location/Qualifiers
1..704
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4995238"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5 kb. Library prepared by Life Technologies."
BASE COUNT 158 a 174 c 214 g 157 t 1 others
ORIGIN
Query Match 95.0%; Score 213.8; DB 10; Length 704;
Best Local Similarity 96.9%; Pred. No. 1.8e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TATTCTTTCTGTGATCTTCAGCAAAGCTTCGGATTCTTCGAGCTGGTCTTTGGCATC 60
|||||
Db 154 TATTCTTTCTGTGATCTTCAGCAAAGCTTCGGATTCTTCGAGCTGGTCTTTGGCATC 213
QY 61 GAGCTGATGGAAGTGACCCCATCGCCAGCGGTGATACATCTTTGCCACCTGGCTGGCCCTC 120
|||||
Db 214 GAGCTGATGGAAGTGACCCCATCGCCAGCGGTGATACATCTTTGCCACCTGGCTGGCCCTC 273
QY 121 TCCTAGATGGCTGCTGGTGTGACATCATGCCAGGACAGCTTCCTGTGATAATC 180
|||||
Db 274 TCCTAGATGGCTGCTGGTGTGACATCATGCCAGGACAGCTTCCTGTGATAATC 333
QY 181 ATCTGCGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
|||||
Db 334 GTCTGCGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 378
RESULT 9
BG765526
LOCUS 602739439F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4869321 5',
DEFINITION mRNA sequence.
ACCESSION BG765526
VERSION BG765526.1 GI:14076179
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 769)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC/DCTD/PTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCMI740 row: n column: 10
High quality sequence stop: 769.
FEATURES
Location/Qualifiers
1..769
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4869321"
/clone_lib="NIH_MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(S). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 161 a 218 c 222 g 168 t
ORIGIN
Query Match 95.0%; Score 213.8; DB 10; Length 769;
Best Local Similarity 96.9%; Pred. No. 1.8e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TATTCTTTCTGTGATCTTCAGCAAAGCTTCGGATTCTTCGAGCTGGTCTTTGGCATC 60
|||||
Db 374 TATTCTTTCTGTGATCTTCAGCAAAGCTTCGGATTCTTCGAGCTGGTCTTTGGCATC 433
QY 61 GAGCTGATGGAAGTGACCCCATCGCCAGCGGTGATACATCTTTGCCACCTGGCTGGCCCTC 120
|||||
Db 434 GAGCTGATGGAAGTGACCCCATCGCCAGCGGTGATACATCTTTGCCACCTGGCTGGCCCTC 493
QY 121 TCCTAGATGGCTGCTGGTGTGACATCATGCCAGGACAGCTTCCTGTGATAATC 180
|||||
Db 494 TCCTAGATGGCTGCTGGTGTGACATCATGCCAGGACAGCTTCCTGTGATAATC 553
QY 181 ATCTGCGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
|||||
Db 554 GTCTGCGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 598
RESULT 10
BM449726
LOCUS AGENCOURT_6392873 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5528433
DEFINITION 5', mRNA sequence.
ACCESSION BM449726
VERSION BM449726.1 GI:18498766
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 872)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC/DCTD/BTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM12205 row: e column: 10
High quality sequence stop: 668.

FEATURES

source Location/Qualifiers

1..872
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5528433"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 186 a 255 c 249 g 182 t
ORIGIN

Query Match 95.0%; Score 213.8; DB 10; Length 872;
Best Local Similarity 96.9%; Pred. No. 1.9e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTCTTCTCGTGCATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGGCATC 60
|||||
Db 507 TATTCTTCTCGTGCATCTTCAGCAAGCTTCCAGTTCCTTGCAGCTGGTCTTTGGGCATC 566
|||||
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGGCACCTGCTGGGCCTC 120
|||||
Db 567 GAGCTGATGGAAGTGGACCCCATCGGCACCTGTACATCTTTGCCACCTGCTGGGCCTC 626
|||||
QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTCTGATATC 180
Db 627 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTCTGATATC 686
|||||
QY 181 ATCTCGGCATTAATCGCAAGAGAGGGGACACTGTGCCCTGAGGAG 225
|||||
Db 687 GTCTGGCCATAATCGCAAGAGAGGGGACACTGTGCCCTGAGGAG 731
|||||

RESULT 11

BM470991 1021 bp mRNA linear EST 05-FEB-2002
LOCUS
DEFINITION AGENCOURT_6478212 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5562971
5', mRNA sequence.

ACCESSION BM470991

VERSION BM470991.1 GI:18520033

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1021)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM12293 row: d column: 12

High quality sequence stop: 725.

Location/Qualifiers

FEATURES

source

1..1021

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5562971"

/clone_lib="NIH_MGC_72"

/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 232 a 290 c 292 g 206 t 1 others
ORIGIN

Query Match 94.6%; Score 212.8; DB 10; Length 1021;

Best Local Similarity 96.4%; Pred. No. 3.7e-46;

Matches 217; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TATTCTTCTCGTGCATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGGCATC 60
|||||
Db 593 TACTTCTTCTCGTGCATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGGCATC 652
|||||

QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
|||||

Db 653 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 712
|||||

QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTCTGATATC 180
|||||

Db 713 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTCTGATATC 772
|||||

QY 181 ATCTCGGCATTAATCGCAAGAGAGGGGACACTGTGCCCTGAGGAG 225
|||||

Db 773 ATCTCGGCATTAATCGCAAGAGAGGGGACACTGTGCCCTGAGGAG 817
|||||

RESULT 12

BM280738

LOCUS

DEFINITION 602401029F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4543566 5',
mRNA sequence.

ACCESSION BM280738

VERSION BM280738.1 GI:13029662

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 934)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMI225 row: i column: 07
High quality sequence stop: 673.

FEATURES

source

1..934

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4543566"

/clone_lib="NIH_MGC_20"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

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BASE COUNT      235 a      266 c      267 g      166 t
ORIGIN
Query Match      90.0%; Score 202.6; DB 10; Length 934;
Best Local Similarity 95.9%; Pred. No. 1.8e-43;
Matches 208; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TATTCTTCTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATC 60
Db 418 TATTCTTCTCTGTGATCTTCAGCAAGCTTCAGTCTCCTTGCAGCTGGTCTTTGGCATC 477

QY 61 GAGCTGATGAAGTGAACCCCAATCGGCCACGTGTACATCTTTGCCACCTGCGCTGGCCCTC 120
Db 478 GAGCTGATGAAGTGAACCCCAATCGGCCACGTGTACATCTTTGCCACCTGCGCTGGCCCTC 537

QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAGACAGCTTCCTGTGATAATC 180
Db 538 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAAGCGACGCTTCCTGTGATAATC 597

QY 181 ATCTGGCCATATCGCAAGAGAGGGCGACTGTGCC 217
Db 598 GTCTGGCCATATCGCAAGAGAGGGCGACTGTGCC 634

RESULT 13
BE541476
LOCUS      BE541476      795 bp      mRNA      linear      EST 09-AUG-2000
DEFINITION 601067928F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454135 5',
            mRNA sequence.
ACCESSION  BE541476
VERSION    BE541476.1 GI:9770121
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM8438 row: h column: 08
            High quality sequence stop: 662.
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                        /clone="IMAGE:3454135"
                        /clone_lib="NIH_MGC_10"
                        /cell_line="MGC36"
                        /lab_host="DH10B"
                        /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                        Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                        Average insert size 1.5 kb. Library prepared by Life
                        Technologies."
BASE COUNT  182 a      199 c      234 g      180 t
ORIGIN
Query Match      89.5%; Score 201.4; DB 10; Length 795;
Best Local Similarity 96.9%; Pred. No. 3.5e-43;
Matches 216; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 3 TTTCTTCTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATCGA 62

BASE COUNT      235 a      266 c      267 g      166 t
ORIGIN
Query Match      90.0%; Score 202.6; DB 10; Length 934;
Best Local Similarity 95.9%; Pred. No. 1.8e-43;
Matches 208; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TATTCTTCTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATC 60
Db 418 TATTCTTCTCTGTGATCTTCAGCAAGCTTCAGTCTCCTTGCAGCTGGTCTTTGGCATC 477

QY 61 GAGCTGATGAAGTGAACCCCAATCGGCCACGTGTACATCTTTGCCACCTGCGCTGGCCCTC 120
Db 478 GAGCTGATGAAGTGAACCCCAATCGGCCACGTGTACATCTTTGCCACCTGCGCTGGCCCTC 537

QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAGACAGCTTCCTGTGATAATC 180
Db 538 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAAGCGACGCTTCCTGTGATAATC 597

QY 181 ATCTGGCCATATCGCAAGAGAGGGCGACTGTGCC 217
Db 598 GTCTGGCCATATCGCAAGAGAGGGCGACTGTGCC 634

RESULT 14
BM015882
LOCUS      BM015882      803 bp      mRNA      linear      EST 30-OCT-2001
DEFINITION 603642276F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5418283 5',
            mRNA sequence.
ACCESSION  BM015882
VERSION    BM015882.1 GI:16530236
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12067 row: g column: 20
            High quality sequence stop: 779.
FEATURES   Location/Qualifiers
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                        /clone_lib="NIH_MGC_87"
                        /tissue_type="mammary adenocarcinoma, cell line"
                        /lab_host="DH10B (phage-resistant)"
                        /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
                        Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                        Average insert size 1.383 kb. Library enriched for
                        full-length clones and constructed by Life Technologies.
                        Note: this is a NIH_MGC library."
BASE COUNT  169 a      236 c      236 g      161 t
ORIGIN
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Best Local Similarity 95.5%; Pred. No. 3.6e-42;
Matches 214; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 TATTCTTCTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATC 60
Db 574 TATTCTTCTCTGTGATCTTCAGCAAGCTTCAGATTCCTTGCAGCTGGTCTTTGGCATC 633

QY 61 GAGCTGATGAAGTGAACCCCAATCGGCCACGTGTACATCTTTGCCACCTGCGCTGGCCCTC 120
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QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAGACAGCTTCCTGTGATAAT 179
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Search completed: September 4, 2002, 16:02:33
Job time: 19343 sec

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Qy 180 CATCTGCGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGG 223
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Db 754 CGTCTGCGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGG 797
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RESULT 15
BE897495
LOCUS 601432326F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917503 5',
mRNA sequence.
ACCESSION BE897495
VERSION BE897495.1 GI:10363014
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 590)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM9744 row: c column: 08
High quality sequence stop: 589.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3917503"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT 133 a 171 c 157 g 129 t
ORIGIN
Query Match 87.5%; Score 196.8; DB 10; Length 590;
Best Local Similarity 92.4%; Pred. No. 5.4e-42;
Matches 207; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy 2 ATTTCCTTCCTGTGATCTTCAGCAAGCTTCGGATCCTTCGACGTGCTTTGGCATCG 61
Db 329 ACTTCCTTCCTGTGATCTTCAGCAAGCTTCGGATCCTTCGACGTGCTTTGGCATCG 388
Qy 62 AGCTGATGGAATGGACCCATCGGCCACGTGTACATCTTTGCCACCTGGGCCCTCT 121
Db 389 AGGTGGTGGAGTGTCCGGCATCGGCCACTTGTACATCCTTGTCACCTGGGCCCTCT 448
Qy 122 CCTACGATGGCTGCTGGGTGACATATCAGATCATGCCAGGACAGGCTTCCTGATAATCA 181
Db 449 CCTACGATGGCTGCTGGGCACAAATCAGATCGTGCCCAAGACAGGCCCTCCTGATAATCG 508
Qy 182 TCCTGGCCCATTAATCGCAGAGAGGGCGACTGTGCCCTGAGGAG 225
Db 509 TCCTGGCCCATTAATCGCAAAAGAGGGCGACTGTGCCCTGAGGAG 552

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